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Sequence 7193, Ap
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/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*/
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/EMC_Celerra_SIDS3/ptodata/2/iaa/RC COMB.pep:*/
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(c) 1993 - 2006 Biocceleration Ltd.
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US-09-968-016-7193
US-09-949-016-9917
US-09-949-016-9917
US-09-949-016-1957
US-09-949-016-1957
US-09-949-016-1957
US-09-949-016-1957
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US-09-172-422-1
US-09-172-422-1
US-10-084-7016-11166
US-10-094-7016-11166
US-10-0949-016-8473
US-09-949-016-8473
US-09-949-016-8474
US-09-949-016-8477
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Maximum Match 100%
Listing first 45 summaries
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Sequence 6644, Application US/09949016

patent No. 6812339

general INCOMPARTION:
APPLICANT: VENTER, U. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
FRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-20
PRIOR PRILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 6844
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US-09-949-016-8472
US-09-949-016-6759
US-09-949-016-6759
US-09-949-016-6759
US-09-949-016-0241
US-10-080-960-34
US-09-949-016-10341
US-09-949-016-10341
US-09-949-016-10382
US-09-538-092-1230
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          ORGANISM: Human
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TYPE: PRT
ORGANISM: Homo sapiens
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| Sequence 7193, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICAMT: VENTER, J. Craig et al.
| APPLICAMT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| CURRENT APPLICATION NUMBER: 00/241,755
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR PLILING DATE: 2000-10-03
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                                                                                                                                                     LIKDFLRNLKBPLLTFRLNRAFWEAARITDEDNSIAAMYQAVGELPQANRDTLAFLMIHL 480
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                                                                               MIPSIVVHCVNEIBQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS
VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTSP
                  301 VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTSP
                                                              MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS
                                                                                                                              LLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHL
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                                                                                                                                                                                                                                                            QFMMVEQENIDPLHVIENSNAFSTPQTPDIKVSLLGPVTTPEHQLLKTPSSSSLSQRVRS
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                                                                                                                                                                                            QRVAQSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLEYWS
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99.6%; Pred. No. 6.7e-99;
tive 0; Mismatches 1;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
Matches 222; Conserv
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ORGANISM: Human
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LENGTH: 245
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RESULT 3 US-09-080-855-2

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Sequence 2, Application US/09080855A

Patent NO. 6083721

GENERAL INFORMATION:

APPLICANT: Saras, Jan

APPLICANT: Franzn, Petra

APPLICANT: Hellman, Ulf

APPLICANT: Hellman, Ulf

APPLICANT: Heldin, Carl-Henrik

TITLE OF INVENTION: PARO, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1

CURRENT APPLICATION WUMBER: US/09/080, 855A

CURRENT FILING DATE: 1998-05-18

EARLIER APPLICATION NUMBER: 08/805,583

SARLIER PILING DATE: 1997-02-25

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FRASEQ for Windows Version 3.0
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9.3%; Score 301; DB 2; Length 1261;
Best Local Similarity 22.4%; Pred. No. 9.4e-19;
Matches 153; Conservative 120; Mismatches 249; Indels 160;
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Sequence 9916, Application US/09949016

Sequence 9916, Application US/09949016

Retent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
PILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 9916

LENTHALES PRICE 
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889 SLQPQDVMCSIGVVDQGCFPKPLLSPEERDIERSMKSLFFSSKEDIHTSESESKIFERAT 948
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Best Local Similarity 25.5%; Pred. No. 3e-17;
Matches 140; Conservative 67; Mismatches 201; Indels 140; Gaps
                                                                                                                                                                                                   | : ||:
| S-----FEESERKQNALGK 962
                                                                                                                                        STLTKNTPRFGSKSKSATNLGR
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APPLICANT: Franza, Petra
APPLICANT: Aspenstrm, Pontus
APPLICANT: Aspenstrm, Ulf
APPLICANT: Heldima, Ulf
APPLICANT: Heldim, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
CURRENT APPLICATION NUMBER: US/09/566,076
CURRENT FILING DATE:
EARLIER APPLICATION NUMBER: 09/080,855
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastsEQ for Windows Version 3.0
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                                                                                                                                                                                                                 ; Sequence 2, Application US/09566076; Patent No. 6475775; GENERAL INFORMATION:
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                                                                                                                                            RESULT 4
US-09-566-076-2
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) ORGANISM: Human
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| Sequence 9917, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| APPLICANT: VENTER, U. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| FILE REFERENCE: CLOOL307 |
| CURRENT APPLICATION NUMBER: US/09/949,016 |
| CURRENT PILING DATE: 2000-04-14 |
| PRIOR APPLICATION NUMBER: 60/241,755 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SEQ ID NO 9917 |
| LEMEGTH: 8338 |
| LEMEGRAPHER OF THE PRIOR P
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Best Local Similarity 25.5%; Pred. No. 3e-17;
Matches 140; Conservative 67; Mismatches 201; Indels 140; Gaps
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LLYYLQHP 820
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ORGANISM: Human
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Sequence 11527, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 00/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          922 SPGLYGFLNVIVHSATGFKQSSNLYCTLEVDSFGYFVNKAKTRVYRDTAEPNWNEEFEIE 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --NSRQLE------PRIETDSVGTPQSNGGMRL-----HDFVSKTVIKPES 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 CVPCGKRIKFG--KLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQ 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                878 ----REQQKKCFRSF------SLTSVBLQMLTNSCVKLQTVHSIPLTINKEDDE 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ORTDHELGKYK
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91 NIPLVPDEBLDALKIKISQIKNDIQRE-KRANKGSKATERLKKKU
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US-09-949-016-6235

Sequence 6235, Application US/09949016

Parent No. 6812339

GENERAL INFORMATION:
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ORGANISM: Homo sapien
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                                                                                             Sequence 7008, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 KLKKREKRRSTSRQFVDGPPGPVKKTRSIGSAVDQ--GNESIVAKTTVTVP-----NDG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----REQOKKCFRSF-----SLTSVELQMLTNSCVKLQTVHSIPLTINKEDDE 905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          960 --ELDPQALQD------RDW-QRTVIAMNG-IEVKLSVKFNSREFSLK---- 997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.6%; Score 278.5; DB 2; Length 1227; 23.5%; Pred. No. 1.2e-16; Live 89; Mismatches 195; Indels 165;
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                                                                                                                                                                                                                      FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 7008
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Best Local Similarity 23.5
Matches 138; Conservative
1259 VOVLLYFLOL 1268
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                                                                               09-949-016-7008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474 AFLMIHLQRVA-QSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLL 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 CGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGE------GMLADFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 LSTIDESGSILSDISFDKTDESLDWDSSLVKTFKLKKREKRRSTSRQFVDGPPGPVKKTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 SIGSAVDQGN-----ESIVAKTTVTVPNDG---GPIEA-VSTIETVPYWTRSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 -IHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTL
                                                                                                                                                                APPLICANT: Carrier, Carrier APPLICANT: Carrier, Carrier APPLICANT: Carrier, Carrier APPLICANT: Carrier, Song APPLICANT: Leng, Song APPLICANT: Melch, Juliet TITLE OF INVENTION: CRANNEL-15 (CNGC-15) POLYNUCLECTIDE GATED TITLE OF INVENTION: CARANNEL-15 (CNGC-15) POLYNUCLECTIDES, POLYPEPTIDES, TITLE OF INVENTION: CARANNEL-15 (CNGC-15) POLYNUCLECTIONS, METHODS, AND USES THEREOF FILE REPERENCE: 200130.442
CURRENT APPLICATION NUMBER: US/09/172,422A
CURRENT APPLICATION NUMBER: US/09/172,422A
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 SQTSPMIPSIVVHCVNBIBQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.3%; Score 270.5; DB 2;
24.4%; Pred. No. 2.4e-15;
:ive 75; Mismatches 203;
Sequence 1, Application US/09172422A Patent No. 6300485 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 24.4%
Matches 130; Conservative
                                                                                 APPLICANT: Adams, Arwen E. APPLICANT: Chiu, Choi Ying APPLICANT: Duhl, David
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APPLICANT: VENTER, J. Craig et al

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678 QDGGTKITPK-----ATN 690
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YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: 199303
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 567 TPDIKV-SLLGPVTTPEHOLL-------KTPSS---
                                                                                                                                                                                                                                                                                                                                            DB 2;
                              FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
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Sequence 10, Application PC/TUS9303076
Sequence 10, Application PC/TUS9303076
GENERAL INFORMATION:
TITLE OF INVENTION: GAP-Associated Protein pl90 and TITLE OF INVENTION: Transduction
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: Granahan, Petricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH192-03A
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-861-8240
TELEFRAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 antino acids
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Patent No. 6979557
GENERAL INFORMATION:
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
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NSVHKLDVSRSPPL 418
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Best Local Similarity
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; ORGANISM: Human
US-09-949-016-11166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 LAPLLVEQCVDFIRERGLIEEGLFRAMPGQANLVRDLQDSF-DCGEKPLFDSTIDVHIVAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 LLKDFLRNLKEPLLTFRLNRAFMEAAEI - TDEDNSIAAMYQAVGELPQANRDTLAFLMI 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479 HLORV-AOSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKROPKVVERLLSLPLE 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 FLDEVQAYSNVNKMSVQNLATVFGPNILRPQV--EDPVT----IMEGTSLVQHLMTVLIR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                538 YWSQFMM--VEQENIDPLHVIENSNAFSTPQ-TPDIKVSLLGPVTTPEHQLLKTPSSSSL 594
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.9%; Score 255; DB 2; Length 585
Best Local Similarity 31.6%; Pred. No. 6.1e-15;
Matches 80; Conservative 43; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.8%; Score 254.5; DB 2; Length 7.6.0%; Pred. No. 1e-14; ive 61; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REPERBING: HI-A0105
FURENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
APPLICANT: NACHANA APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGAHARI, KEMII
APPLICANT: NAGAHARI, KEMII
APPLICANT: MASUHO, YASUHIKO
TITLE REFERENCE: 048435/0160
CURRENT APPLICATION NUMBER: US/10/094, 749
CURRENT PILING DATE: 2002-03-12
PRIOR PILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PARENTIN VUMBER: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 2336, Application US/10104047; Patent No. 6943241; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : |:: |
288 DGAAVAVLSRTAP 300
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Best Local Similarity 26.0%
Matches 113; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    595 SQRVRSTLTKNTP
                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-094-749-1841
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US-10-104-047-2336
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LENGTH: 589
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ABBURALL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OP DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OP DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OP DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 00/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SPRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|:::| | |: :::| TRERKKKFEKDGERPYSLIDRHIHLSSKKKESQLQBADLQVDKERHNFFESSLDYVYQIQ 134
                                                                                                                                                                                                                                                                                                                                  336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TDEDNSIAAMYQAVGELPQANRDTLAFLMIHLQRV-AQSPHTKMDVANLAKVFGPTIV 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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-RLHDFVSKTVIKPESCV 301
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                                                                                                                                                                                                                                                                                                    29 INIAESFKEF------AELLINEVENERMMYHNASDLLIKPLENFRKEQIGF 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 FLPGNKVSEHPCNEE-NPGKFLFEVVPGGDRDRMTANHESYLLMASTQNDMEDW--VKSI
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illarity 22.2%; Pred. No. 1.1e-14;
Conservative 111; Mismatches 235; Indels 196;
        256 NSDSTLNSROLEPRTETDSVGTPQSNGGM-
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Patent No. 6812339
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--TVPLLSKVDDIHAIČSLLKDFLENLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAV 462
                                                                                                                                                                                                                                                                                                                                                                                378 PGDVDFHNSDWDIKTITSSLKFYLRNLSEPVMTYRLHKELVSAAKSDNLDYRLGAIHSLV 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 EVQE---SKKFNIVEPVLAFLHSLFISNSLTVELTQDFLPYKQQL--QLSLQNTRNHFSS 189
                                                                                                                                          232 WVKYYCQYEKETKTL-----TMTPMEQKP-----GAKQGPLDLTLKYCVRR---KT 274
                                                                                                                                                                                                  ------ECRDRCPLPCI---PTLIGTPVK 345
                                                                                                                                                                                                                                     ES---IDKRF-----CFDIETNERPGTITLQALSEANRKLWMEAMDGKEPIYHSPIT 323
                                                                                                                                                                                                                                                                             346 IGEGMLADFVSQTSPMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVK- 404
                                                                                                                                                                                                                                                                                                      324 KQQEMELNEVGF-----KFVRKCINIIETKGIKTEGLYRTVGSNIQVQKLLNAFFDPKC 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    561 AFSTP-----KTPSS---- 591
                                       ---VSTIE 237
                                                                                                                    238 TVPYWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKP 297
                                                                            ---APOTCKLP--GOPTIEGYLYTQEKWALGIS
                                     SRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGP-IEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORMATION:
APPLICANT: Milennium Pharmaceuticals, Inc.
APPLICANT: Milennium Pharmaceuticals, Inc.
APPLICANT: Glucksmann, Maria
APPLICANT: Glucksmann, Maria
APPLICANT: Glucksmann, Maria
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 80090, 52874,52880,63497,AND 33425
TITLE OF INVENTION: METHODS AND CORPOSITIONS OF HUMAN
TITLE OF INVENTION: METHODS AND USES THEREOF
FILE REFERENCE: 3815-2004.00
CURRENT FILING DATE: 2001-10-19
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/242,038
PRIOR PLICATION NUMBER: US 60/242,038
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ 1D NOS: 37
SOFTWARE: FRESERG for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           609 KLEPCPEVDVGKLVSRLQDGGTKITPK-----ATN 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SSLSQRVRSTLTKNTPRFGSKSKSATN 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIKROPKVVERLLSLPLEYWSQFMM--VEQENIDPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Consensus amino acid US-10-080-960-32
                                                                                                                                                                                                298 ESCVPCGKRIKFGKLSLKCRDCRVVSHP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32, Application US/10080960 Patent No. 6979564
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                                                                        TREEMEELKKRMKE-
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Score 251; DB 2; Length 170; Pred. No. 1.8e-15;

Query Match 7.7%; Best Local Similarity 39.8%;

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5
                        363 PSIVVHCVNEIE-----QRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVD--- 413
                                                                                       414 -DIHAICSLIKDFLRNLKEPLLTFRLNRAFMEAA--EITDEDNSIAAMYQAV-GELPQAN 469
                                               9
                                       18; Gaps
 52; Indels
                                                                                                                       470 RDTLAFLMIHLQRVAQ----SPHTKMDVANLAKVFGPTIV 505
                                                                                                                                       27; Mismatches
 64; Conservative
 Matches
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Search completed: August 9, 2006, 16:23:32 Job time : 53 secs Sequence 185, App Sequence 531, App Sequence 531, App Sequence 725, App Sequence 725, App Sequence 724, App Sequence 121, App Sequence 731, App Sequence 731, App Sequence 731, App Sequence 730, App Sequence 278, App

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Sequence:

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DNA molecules encoding them and their use in
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            US-10-756-149-5188
US-10-499-065A-531
US-10-087-192-333
US-10-153-668-212
US-10-153-668-212
US-10-153-668-710
US-10-153-668-710
US-10-072-012-731
US-10-072-012-731
US-10-072-012-731
US-10-072-012-730
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US-10-072-012-280
US-10-072-012-278
US-10-072-012-278
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APPLICANT: Glotzer, Michael
APPLICANT: Glotzer, Michael
APPLICANT: Mishima, Aber
APPLICANT: Mishima, Masanori
APPLICANT: Kaitna, Susanne
TITLE OF INVENTION: Cyk-4 polypeptides, DNA n
TITLE OF INVENTION: Greening methods
FILE REFERENCE: 0652.2260001/EKS/AES
CURRENT APPLICATION NUMBER: EP 00 112 880.0
FRIOR APPLICATION NUMBER: EP 00 112 880.0
PRIOR APPLICATION NUMBER: EP 01 110 554.1
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 60/241,231
PRIOR FILING DATE: 2000-10-430
PRIOR APPLICATION NUMBER: 60/241,231
PRIOR APPLICATION NUMBER: C0/241,231
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PRIOR APPLICATION NUMBER: C0/241,231
SRIOR FILING DATE: 2000-10-18
SRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.1
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Patent No. US20020076785A1
GENERAL INFORMATION:
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Sequence 1106, App
Sequence 5722, App
Sequence 427, Appl
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Sequence 1045, App
Sequence 1046, App
Sequence 45186, App
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Sequence 50263, Appl
Sequence 6263, Appl
Sequence 6388, Appl
Sequence 638, Appl
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TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: RECUMANION ARTHRITIS
TITLE OF INVENTION: RECUMANION ARTHRITIS
FILE REPERENCE: 10872.514696
CURRENT PILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/336,220
PRIOR APPLICATION NUMBER: US 60/336,220
PRIOR PILING DATE: 2001-10-31
SOFTWARE: FREESE FOR FOR WINDOWS VERSION 4.0
SEQ ID NO 1106
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Pred. No. 9.6e-258;
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                     YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC
                                       YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC
                                                                                                         VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTSP
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Sequence 408, Application US/10287436A

PUDICATION. US/2005020421A1

GENERAL INFORMATION:

APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER

ITILE OF INVENTION: RHEUMATOID ARTHRITIS

FILE REFERENCE: 10872.514696

CURRENT APPLICATION NUMBER: US/10/287,436A

CURRENT PILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: US 60/336,220

PRIOR FILING DATE: 2001-10-31
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99.8%; Score 3237; DB 5;
Best Local Similarity 99.8%; Pred. No. 9.6e-258;
Matches 631; Conservative 0; Mismatches 1;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 408
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ORGANISM: Homo sapiens
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US-10-287-436A-408
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Sequence 5722, Application US/10756149

Sequence 5722, Application Wo. US20050181375A1

GENERAL INFORMATION:
ALSO MATABLA MATHONS OF SCREENING FOR MODULATORS OF METASTATIC CANCER, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER FILE REPERRENCE: file
CURRENT APPLICATION NUMBER: 2004-01-12

NUMBER OF SEQ ID NOS: 5818

SOFTWARE: PARENTIN VERSION 3.2

SEQ ID NO 5722

LENGTH: 632
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                                                MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS
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Pred. No. 3.6e-257;
0; Mismatches 2;
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Best Local Similarity
Matches 630; Conserv
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US-10-756-149-5722
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GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Secritst, Heather
APPLICANT: Monach, Raodon
APPLICANT: Indirias, Carol Y.
APPLICANT: Indirias, Carol Y.
APPLICANT: Pan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG
TITLE OF SECRET APPLICATION NUMBER: 12001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 3.6e-257;
0; Mismatches 2;
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; Patent No. US20020068288A1
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Best Local Similarity 99.7%;
Matches 630; Conservative 0
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CORGANISM: Homo sapiens
US-09-833-790-413
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US-09-833-790-413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 MAVEQENIDPLHVIENSNAFSTPQTPDIKVSLLGPVTTPEHQLLKTPSSSSLSQRVRSTL
KAETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSE
                                                 VAQSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLBYWSQF
                                                                                                                    MMVEQENIDPLHVIENSNAFSTPOTPDIKVSLLGPVTTPEHQLLKTPSSSSLSQRVRSTL
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84.4%; Pred. No. 3e-216;
                                                                                                                                                                                                        541 TKNTPRFGSKSKSATNLGRQGNFFASPMLK 570
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Janesch-Plunger, Verena APPLICANT: Romano, Alper APPLICANT: Romano, Alper APPLICANT: Romano, Alper APPLICANT: Rainna, Masanori APPLICANT: Kainna, Susanne TITLE OF INVENTION: Cyk-4 polypeptides, DNA my TITLE OF INVENTION: Screening methods TITLE REPRENCE: 0652.226001/EKS/AES CURRENT FILING DATE: 2001-06-19 PRIOR APPLICATION NUMBER: EP 01 112 880.0 PRIOR APPLICATION NUMBER: EP 01 110 554.1 PRIOR APPLICATION NUMBER: EP 01 110 554.1 PRIOR FILING DATE: 2001-04-30 PRIOR PILING DATE: 2001-04-30 PRIOR PILING DATE: 2000-10-18 PRIOR PILING DATE: 2000-10-18 PRIOR FILING DATE: 2000-10-18 PRIOR FILING DATE: 2001-06-13 SOFTWARE: PARCHING DATE: 2001-06-13 NUMBER OF SEQ ID NOS: 6 SEQ ID NOS: 6 LENGTH: 628
                                                                                                                                                                                     TKNTPRFGSKSKSATNLGRQGNFFASPMLK 632
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                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09881736
Patent No. US200200016785A1
GENERAL INFORMATION:
APPLICANT: Glotzer, Michael
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Best Local Similarity 84.4%
Matches 534; Conservative
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; ORGANISM: Mus musculus
US-09-881-736-4
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KDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHLQR 482
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                                                   LIKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHL
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Patent No. US20020068288A1

GREKRAL INFORMATION:

APPLICANT: Lodges, Michael J.

APPLICANT: Mang, Tongtong

APPLICANT: Mang, Tongtong

APPLICANT: Momath, Raacher

APPLICANT: Momath, Raacher

APPLICANT: Momath, Raacher

APPLICANT: Momath, Raach

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.512

CURRENT APPLICATION NUMBER: US/09/833,790

CURRENT FILING DATE: 2001-04-11

NUMBER OF SEQ ID NOS: 440

SOFTWARER: FESTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2919; DB 3; Length 570;
Pred. No. 1.4e-231;
0; Mismatches 1; Indels
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Best Local Similarity 99.8%;
Matches 569; Conservative (
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                                                                         SLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIH 479
                                                                                                                                                                          SLIKDFIRNIKEPILITFWISKAFWEAAEITDEDNSTAAMYQAVSELPQANRDTLAFLMIH 480
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CVPCGKRIKFGKLSLKCRDCRLVSHPECRDRCPLPCIPPLVGTPVKIGEGMLADFVSQAS 360
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                                                                                                                                                                                                                                                                             LORVSQSPDTKMDIANLAKVFGPTIVAHTVPNPDPVTMFQDIKRQLKVVERLLSLPLEYW
                                                                                                                                                                                                                                                LQRVAQSPHTKMDVANLAKVFGPT1VAHAVPNPDPVTMSQD1KRQPKVVERLLSLPLEYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1045, Application US/10408765A
| Publication No. US20040101874A1
| GENERAL INFORMATION:
| APPLICANT: Ghosh, Soumitra S. |
| APPLICANT: Tang, Bing |
| APPLICANT: Tang, Bing |
| APPLICANT: Gibson, Bradford W. |
| APPLICANT: Glenn, Gary W. |
| APPLICANT: Warnock, Dale B. |
| APPLICANT: Glenn, Gary W. |
| APPLICANT: Warnock, Dale B. |
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Pred. No. 8.4e-89;
0; Mismatches 2;
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12-11-097-143-30960
1 Sequence 30960, Application US/11097143
; Publication No. US20050208558A1
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hes 234; Conservative
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ORGANISM: Homo sapiens
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US-10-408-765A-1045
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US-10-408-765A-1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 VGQGAERFCATIKVIIPQDGQGVIRAESTIESLPVIAGNERIGDGLSSTPRRSVLKEATA 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEEQK 122
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                                     NUCLEIC ACID
EXPRESSION OF 10,000 OR MORE
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Best Local Similarity 35.1%; Pred. No. 5.9e-62;
Matches 228; Conservative 110; Mismatches 225; Indels
APPLICANT: VELLE, O. LIBY
APPLICANT: VELLE, O. LIBY
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC
TITLE OF INVENTION: ARRANS, FOR DETECTING EXP
TITLE OF INVENTION: ARRANS, FOR DETECTING EXP
TITLE OF INVENTION: ARRANS.
FILE REPERENCE: CLOOO728
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/15/832
PRIOR PILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/16(,191
PRIOR PILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-11-28
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-28
PRIOR PILING DATE: 1999-11-28
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-24
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FRASISE FOR WINDOWS VERSION 4.0
SEQ ID NO 30360
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; OTHER INFORMATION: Reverse transcriptase domain identified by PFam, accession
; OTHER INFORMATION: name rvt, E-value=6e-15, PFam score of 63.1
US-10-450-763-40589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (57)...(100)
TOTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by OTHER INFORMATION: eMATRIX, accession number DM01354T, p-value=1.000e-40, OTHER INFORMATION: 9.48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | :: | :: | :: | :: | :: | :| 460 IYNELKKQIYKKKTNNPIKKWTNDMNRHFSKEDIYAAKKHMKKCSSLPAIREWQIKTTWRY
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                                                                                                                                                                    Sequence 40589, Application US/10450763

Publication No. US20050196754A1

GENERAL INCORMATION:

APPLICANT: Hyseq. Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790C193/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: 09/540,117

PRIOR PLILING DATE: 2000-03-31

PRIOR PLILING DATE: 2000-03-31

PRIOR PLILING DATE: 2000-03-31

PRIOR PLILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR PLILING DATE: 2000-03-31

PRIOR PLILING DATE: 2000-03-31

SPRIOR PLILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR PLILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167
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46.9%; Pred. No. 1.3e-41;
tive 35; Mismatches 68;
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US-10-450-763-50263
; Sequence 50263, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION;
; APPLICANT: Hyseq, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.99
Matches 153; Conservative
4309 RLPSLPLEYW 4318
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ORGANISM: Homo sapiens
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NAME/KEY: DOMAIN
                                                                                                                 RESULT 11
US-10-450-763-40589
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OTHER INFORMATION: 7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE domain identified
OTHER INFORMATION: by eMATRIX, accession number DM00895E, p-value=3.333e-11, raw scd
OTHER INFORMATION: of 15.72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKVDDIHAICSLLKDFLRNFKEPLLTFRLNKAFMEAAEITDEDNSISAMYQAVGELPQAN 4248
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       AKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLEYWSQFMMVEQENIDPLHVI 556
                                              SKVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------RGLTETGLY----RISGCDR--TVKELKEK-FLRVKTVPLL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85; Indels 132;
                                                                                                                                                                                               216 VAKTTVTVPNDGGPIE-----AVSTIETVPYWTRSR-----RKTGTLQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 CPLPCIPTLIGTPVKIG-----EGMLADFVSQTSPMIPSIVVHCVNEIEQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.3%; Score 625; DB 5; Length 4318; llarity 38.8%; Pred. No. 6.4e-41; Conservative 46; Mismatches 85; Indels 13:
                                                                                                                                                            -----EHQLLKTPSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hyseq, Inc.
TITLE OF INVERTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES; TITLE ACIDE AND POLYPEPTIDES; TITLE ACIDE AND POLYPEPTIDES; CURRENT APPLICATION NUMBER: US/10/450,763; CURRENT APPLICATION NUMBER: PCT/US01/08631; PRIOR APPLICATION NUMBER: PCT/US01/08631; PRIOR APPLICATION NUMBER: 09/540,217; PRIOR FILING DATE: 2000-03-31; PRIOR APPLICATION NUMBER: 09/649,167; PRIOR FILING DATE: 2000-08-23; NUMBER OF SEQ ID NOS: 60736; SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PWNSDSTLNS-----RQLE----PRTETDS-
                                                                                                                                                557 ENSNAFSTPQT-----PDIKVSLLGPVTTP-
                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 45146, Application US/10450763; Publication No. US20050196754A1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-450-763-45146
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (190)..(435)
OTHER INPORMATION: *W TRANSCRIPTASE REVERSE II ORP2 domain identified by
OTHER INFORMATION: ematrix, accession number DM01354N, p-value=1.000e-40, raw score of the information: 13.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELSIA INC. DESCUSSION:
APPLICANT: Glotzer, Michael
APPLICANT: Glotzer, Michael
APPLICANT: Glotzer, Michael
APPLICANT: Massanori
APPLICANT: Kaitna, Susanne
TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use in
TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use in
FILE REFERENCE: 0652.2260001/EKS/ABS
CURRENT APPLICATION NUMBER: US/09/881,736
CURRENT FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1029 FKEPLLTFRLINKAFMEAAEITDEDNSISAMYQAVGELPQANRDTLVFLMIHLQRVAQSPY 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   429 LKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHLQRVAQSPH 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------TAKETTIRVNRO 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SKVDDIHAICSLLKDFLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 WTRSRRKTGTLQPWNSDST-LNSR----QLEPRTETDSVGTPQSNGGMRLH-----DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290 VSKTVIKPESCVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489 TKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKROPKVVERLLSLPLEYW 539
                                                                                                                                                                                                                                                                                                                                                                                                                                        84;
                                                                                                                                                                                                                                                                                                                                                                                          Length 1139;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 19.1%; Score 618; DB 5; Length 11 Best Local Similarity 45.0%; Pred. No. 3e-41; Matches 158; Conservative 39; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     875 MSKT---PKAMATKTKIDKWDLIQLKSFFC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 ----EGMLADFVSQTSPMIPSIVVHCVNEIEQ---
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PRIOR PELING DATE: 2000-06-19
PRIOR PELING DATE: 2000-06-19
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
PRIOR PILING DATE: 2000-10-18
PRIOR PILING DATE: 2000-10-18
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09881736 Patent No. US20020076785A1
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                           NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 44317
LENGTH: 1139
                                                                                                                                                                                                                                                                                                                                         US-10-450-763-44317
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LOCATION: (354)..(379)
LOCATION: (354)...(379)
THER INFORMATION: 7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE domain identified
OTHER INFORMATION: by eMATRIX, accession number DM00895E, p-value=3.667e-11, raw
OTHER INFORMATION: of 15.72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (315)...(600)

, OTHER INFORMATION: Reverse transcriptase domain identified by PFam, accession
, OTHER INFORMATION: name rvt, E-value=2.8e-64, PFam score of 227.0
US-10-450-763-50263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 WNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESCVPCGKRIKFGKLSL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 KCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIG-----EGMLADFVSQTSPMIPSIVVH 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 CVNEIEQ-------RGLTETGLY----RISGCDR--TVKELKEK-FLRV 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.1%; Score 618; DB 5; Length 1086; 46.9%; Pred. No. 2.8e-41; tive 35; Mismatches 68; Indels 7
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP2/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT PILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 50263
LENGTH: 1086
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; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyee, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES; FILE REFREBNCE: 790CTP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-03-31
; PRIOR PLING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: DOMAIN
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US-10-450-763-44317
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                                                                                                                                                                  119
                                                                                                                                                                                       EQKSALAFLINRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWD---SSLVKTFK 176
                                                                                                                                                                                                                                                                                                    ------RQFVDGPPG----PVKK 200
                                                                                                                                                                                                                                                                                                                                       246
                                                                                                                                                                                                                                                                                                                                                                     201 TRSIGSAVDQGNESIVAKTTVT-----VPNDGGP------IEAVSTIETVP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                         241 YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGWRLHDFVSKTVIKPESC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIP-----TLIGTPVKIGEGM 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKCATALKLA-TSMKCRDCHQVVHRSCCNKLHLPCIPRPKTWMTPKSALRGAKPGAGEFR 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 KVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEI--TDEDNSIAAMYQAVGELPQA 468
                                                                                                                                                                                                                                                                    132 EDRDQFKFLHE---PLVRTYSKRVQ--QRHPHLMEDTQDDEDDSEVDYDETGDSFEEVIH 186
                                                                                                                     14 NSRHIFNMILNSQRPQFDIKDIGMFHLIDEIERLRKLWKDSEESKKKLNADWREAEEALA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLO00728
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: 60/11/93,143
CURRENT PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-10-10
PRIOR PULING DATE: 1999-10-10-10
                                                                                                                                                                                                                                                                                                                            | : | | : : | | : : | | 307 GQTTNNIGLGMSSAILTKSTLDIRTLKRGTPAWTNGTTR-DIAMRPHTFIEAGIKAMRKC
                                                                                                NVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKW------QRTDHELGKYKDLLM
                                                                                                                                                                  KAETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSE
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                                                                  Gaps
                                                                Indels 121;
                                 Length 681;
                               Query Match 16.7%; Score 541.5; DB 3; Best Local Similarity 25.9%; Pred. No. 2.8e-35; Matches 180; Conservative 109; Mismatches 285;
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pvtt----spatpllarsanatrargahllgs
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                                                                                                                                                                                                                                                                                                       LKK-REKRRSTS-------
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US-11-097-143-4533
US-09-881-736-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 QSNGG-MRLHDFVSKT-VIKPESCVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 OSHSGLLREHNFKIKSYYYNVGNCVHCRKRIRFAMASLRCRACPLRCHIGCCRQLTVNCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 384;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 LTLENVVTWQRVLKVLLLMPAGFWSQFLEV 336
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PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: PASISEQ for Windows Version 4.0
SOFTWARE: 984533
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                                                                                                                                                                                                                                                                                                                                                                                                                                    14.78;
40.78;
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Best Local Similarity 40.73
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-4533
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Sequence 41184, A
Sequence 4817, Ap
Sequence 41178, A
Sequence 2, Appli
Sequence 23, Appli
Sequence 2, Appli
Sequence 23, Appli
Sequence 2, Appli
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3026, Ap
3026, Ap
4126, Ap
14, Appl
49978, A
50683, A
50683, A
5083, A
5083, A
5083, A
11, Appl
15, Appl
15, Appl
16, Appl
16, Appl
17, Appl
18, Appl
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12, Appl
13, Appl
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16, Ap
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1 MDTWMLNVRNLFEQLVRRVE.....SKSATNLGRQGNFFASPMLK 632
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-293-697-4817
US-10-49-902-41178
US-11-265-052-23
US-11-265-065-23
US-11-265-065-23
US-11-293-697-3665
US-11-293-697-3665
US-10-293-697-3026
US-10-293-697-3026
US-10-293-697-3026
US-10-293-697-3026
US-10-480-962-14
US-10-480-962-14
US-10-480-962-14
US-10-480-902-46157
US-10-49-902-46157
US-10-49-902-46157
US-10-49-902-46157
US-11-251-465-31
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US-11-293-697-2967
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 44450, A Sequence 1, Appli Sequence 157, Appli Sequence 157, Appli Sequence 157, Appli Sequence 32, Appli Sequence 32, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10212, Appli Sequence 10211, A Sequence 10211, A Sequence 10211, A Sequence 4764, A Sequence 84764, A Sequence 84764, A Sequence 41600, A Sequence 66, Appli
US-10-449-902-44450 US-10-544-944-1 US-11-293-349-8779 US-11-293-349-8779 US-10-449-902-1558 US-10-449-902-51958 US-11-251-643-8 US-11-259-950-8 US-11-259-950-8 US-11-354-079-22 US-11-354-079-22 US-11-354-079-22 US-11-354-079-22 US-11-354-079-22 US-11-354-079-22 US-11-354-079-22 US-11-354-079-22 US-11-354-079-22 US-11-354-079-22 US-11-353-349-10211 US-11-056-3558-84765 US-11-056-3558-84765 US-11-056-3558-84765
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                                                                                                                                                                                                                                360 PMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPL--LSKVDDIHA 417
                                                                                                                                                                                                          418 ICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSI--AAMYQAVGELPQANRDTLAF 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLKDFLRNLKEPLLTFRLNRAFMEAAEI--TDEDNSIAAMYQAVGELPQANRDTLAFLMI 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLQRV-AQSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLE 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 FLDEVQSYSGVNKMSVQNLATVFGPNÍLRPKV--EDPLT----ÍMEGTVVVQQLMSVMIS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538 YWSQFMMVEQE-NIDPLHVIENSNAFSTPQTPDIKVSLLGPVTTPEHQLLKTPSSSSLS- 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 KHDCLFPKDAELQSKPQDGVSNNNEIQ-----KKATMGQLQNKENNNTKDSPSRQCSW 281
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Sequence 41178, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
                                                                                                                                                                                                                                                                                                                  1108 LVLHLYRVQERSVDNRMNARNLGVVFGPTLMRSADPSQE 1146
                                                                   308 KFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEG--
                                                                                                                                                                                                                                                                                 LMIHLORVAQ-SPHTKMDVANLAKVFGPTIVAHAVPNPD 513
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29.4%; Pred. No. 1.8e-08;
:ive 45; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4817, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELLY RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR PILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver: 2.1
SROLEPRIEIDSVG--TPOSNGG-----
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Best Local Similarity 29.48
Matches 83; Conservative
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US-11-293-697-4817
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
TILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR PELING DATE: 2002-05-30
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 RKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFV-----SKTV
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; Sequence 2, Application US/11265052
; Sequence 2, Application US/11265052
; Publication No. US20060104982A1
; GENERAL INFORMATION:
; APPLICANT: University of Texas, Board of Regents
; TITLE OF INVENTION: THERAPIES FOR SEIZURE DISORDERS USING RLIP76
; FILE REPERENCE: 124263-1038
; CURRENT APPLICATION NUMBER: US/11/265,052
; CURRENT PILING DATE: 2003-11-02
; PRIOR APPLICATION NUMBER: 10/714,506
; PRIOR FILING DATE: 2003-11-13
; PRIOR FILING DATE: 2003-11-13
; PRIOR PILING DATE: 2003-11-13
; PRIOR PILING DATE: 2003-11-13
; PRIOR PILING DATE: 2004-11-13
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; ORGANISM: Oryza sativa
US-10-449-902-41178
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US-11-265-065-2
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                                                                                                                                                                                                                                                                                           118 SEEQKSALAF---LNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWDSSLVKT 174
                                                                                                                                                                                                                                                                                                                                                                                 175 FKLKKREKRRSTSRQFVDGPPG-----PVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGP 229
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## Publication No. US20060104982A1
## GENERAL INFORMATION:
## APPLICANT: University of Texas, Board of Regents
## TITLE OF INVENTION: THERAPIES FOR SEIZURE DISORDERS USING RLIP76
## FILER REFRENCE: 124263-1038
## CURRENT APPLICATION NUMBER: US/11/265,052
## CURRENT FILING DATE: 2005-11-02
## PRIOR APPLICATION NUMBER: 10/714,506
## PRIOR PLICATION NUMBER: 10/713,578
## PRIOR PLICATION NUMBER: 0/713,578
## PRIOR PLICATION NUMBER: 60/425,917
## PRIOR PPLICATION NUMBER: 60/425,917
## PRIOR PLILING DATE: 2002-11-13
## PRIOR PLILING DATE: 2003-11-13
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                                                                                                                                                                                               ch 7.1%; Score 229.5; DB 7; Length I Similarity 22.9%; Pred. No. 2.9e-07; 92; Conservative 69; Mismatches 146; Indels
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                  NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.3
SRQ ID NO 2
LENGTH: 655
TYPE: PRT
ORGANISM: homo sapiens
PRIOR FILING DATE: 2002-11-13
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; ORGANISM: homo sapiens
US-11-265-052-23
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Best Local S
Matches 92
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118 SEEQKSALAF---LNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWDSSLVKT 174

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Sequence 2, Application US/11265065

Sequence 2, Application US/11265065

Sequence 2, Application US/11265065

Publication No. US20060104983A1

GENERAL INFORMATION:

APPLICANT: University of Texas, Board of Regents

TITLE OF INVENTION: THERAPIES FOR THE REGULATION OF INSULIN AND GLUCOSE USING RLIP76

FILE REPERENCE: 124263-1039

CURRENT APPLICATION NUMBER: US/11/265,065

CURRENT PILING DATE: 2003-11-02

PRIOR PILING DATE: 2003-11-13

FRIOR PILING DATE: 2003-11-13

PRIOR PILING DATE: 2003-11-13

PRIOR APPLICATION NUMBER: 60/425,917

FRIOR APPLICATION NUMBER: 60/425,917

PRIOR RILING DATE: 2002-11-13

PRIOR PILING DATE: 2002-11-13
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29 SSERISPTKFPGLYRTGEPSPPH-----DILHEPPDVVSD---DEKDHG-----KKK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 IEAVSTIETVPYWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDF
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Best Local Similarity 27.6%; Pred. No. 6.5e-07;
Matches 80; Conservative 54; Mismatches 130; Indels
US-11-293-697-3665
Sequence 3665, Application US/11293697
Sequence 3665, Application US/11293697
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT PILING DATE: 2005-12-05
PRIOR FILING DATE: 2005-12-05
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PARCELING DATE: 2005-12-05
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Publication No. US20060105376A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel full length cDNA
FILE REPERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR FILING DATE: 2002-13-28
NUMBER OF SEQ ID NOS: 5458
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SEQ ID NO 3026
LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3665
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 73; Conserv
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Sequence 23, Application US/11265065

Publication No. US20060104983A1

GENERAL INFORMATION:

APPLICANT: University of Texas, Board of Regents

TITLE OF INVENTION: THERAPIES FOR THE REGULATION OF INSULIN AND GLUCOSE USING RLIP76

FILE REFERENCE: 124263-1039

CURRENT APPLICATION NUMBER: US/11/265,065

CURRENT FILING DATE: 2005-11-02

PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2003-11-13

PRIOR PILING DATE: 2002-11-13

PRIOR PILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13
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                                            406 VPLLSKVDDI - - HAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVG 463
                                                                                                                                                       118 SEEQKSALAF---LNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWDSSLVKT 174
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Best Local Similarity 22.9%; Pred. No. 2.9e-07;
Matches 92; Conservative 69; Mismatches 146; Indels
                                                                                                                                                                                                                                                               ELPOANRDTLAFLMIHLORV-AQSPHTKMDVANLAKVFGPTI 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.3 SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-265-065-23
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107 ILTILCLKGPSTEGIFRRAANEKARKELKEELNSGDAVDLERLP-----VHLLAVVFK 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----VLSWPFLMRRLSPASDFSGALETDLK---ASLFDQPLSIICGDSDTLPRPIQD 106
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                  256 NSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC--VPCGKRIKFGKLS 313
                                                                                                     314 LKCRDCRVVSHPECRDR-CPLPCIPTLIGTPVKIGEGMLAD----FVSQTSPMIPSIVVH 368
                                                                                                                                               -----VLSWPFLMRRLSPASDFSGALETDLK---ASLFDQPLSIICGDSDTLPRPIQD 106
                                                                                                                                                                                                                                                                                      DFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHLQRV 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 ATAAGLDSAGPQDAREVSPEPIVSTVARLKSSLAQPDRRYSEPSMPSSQECLESRVTNQT 396
                                                                                                                                                                                                                                                                                                                                                                                                          160 DFLRSIPRKLLSSDLFEEWMGALEMQDEEDRIEALKQVADKLPRPNLLLLKHLVYVLHLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540 SQFMMV------EQENIDPLHVIENSNAFSTPQTPDIKVSLLGPVTTPEHQ----
                                                 369 CVNEIEQRGLTETGLYRISGCDRTVKELKEKF----LRVKTVPLLSKVDDIHAICSLLK
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22.1%; Pred. No. 7e-05;
tive 78; Mismatches 154; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4126, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; PILE REPERENCE: H1-A0106
; CURRENT PELLOGATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR SEQ ID NOS: 5458
; NUMBER OF SEQ ID NOS: 5458
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Best Local Similarity 22.1%
****heg 97; Conservative
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CORGANISM: Homo sapiens
US-11-293-697-4126
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                                        78 OLLMNHLANVANNHKONLMTVANLGVVFGPTLLR---POSETVAAIMDIKFONIVIEILI 134
                                                                                       -----BLPLEYWSQFMMVEQENID-----PL---HVIENSNAFSTPQTPD 569
                                                                                                                   192 IINSSLESVSSNPNSILN--SSSSLQPNMNSSDPDLAVVKPTRPNSLPPNPSPTSPLSPS 249
474 AFLMIHLQRVAQS-PHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLL
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22.1%; Pred. No. 7e-05;
iive 78; Mismatches 154; Indels 110;
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APPLICANT: RALCHARDON, INDES
TITLE OF INVENTION: INTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: PF-1002 USN
CURRENT APPLICATION WURBER: USN
CURRENT APPLICATION WURBER: PCT/USO2/17955
PRIOR PRIOR PELING DATE: 2003-12-04
PRIOR PILING DATE: 2003-06-06
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-20
PRIOR PILING DATE: 2001-06-20
PRIOR PILING DATE: 2001-06-20
PRIOR PILING DATE: 2001-06-20
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-39
PRIOR PILING DATE: 2001-06-39
PRIOR PILING DATE: 2001-06-39
PRIOR PILING DATE: 2001-07-06
PRIOR PILING DATE: 2001-07-06
PRIOR PILING DATE: 2001-07-06
PRIOR PILING DATE: 2001-07-06
PRIOR PILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T: YANG, Junming; EMERLING, Brooke M.;
T: TANG, Y. Tom; BAUGHN, Mariah R.;
T: LEE, Ernestine A.; RANKUMAR, Jayalaxmi;
T: YUE, Henry; GRIFFIN, Jennifer A.;
T: CHAWLA, Narinder K.; TRAN, Bao
T: NGUYEN, Danniel B.; KHAN, Farrah A.;
T: SWARNHI, Ameena R.; HAFALIA, April J.A.;
T: SWARNHEN, Anita; GURURAJAN, Rajagopal;
T: POLICKY, Jennifer L.; YAO, Monique G.;
T: WARREN, Bridget A.; GIETZEN, KIMDELY J.;
T: SANNANWALA, Bharati, HONGHELL, Cynthia D.;
                                                                                                                                                                                                                                                                                             606 TPRFGSKSK------SATNLGRQGN 624
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RICHARDSON, Thomas W.; LEE, Sally;
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US-10-480-962-13
                                                                                                                                                                            570 IKVSLLGPVTTPEHQLLKTPSSSSLSQRVRST-
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/10480962
Publication No. US20060115813A1
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Best Local Similarity 22.1%
Matches 97; Conservative
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SEQ ID NO 13
LENGTH: 731
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54; Conservative
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OTHER INFORMATION: Xaa
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ORGANISM: Homo sapien
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US-10-322-836-48
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                   184 AQ-SPHTKMDVANLAKVFGPTIVAHAVPNPDPVTM--SQDIKRQPK-VVERLLSLPLEYW 539
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                                                                                                                               337 ATAAGLDSAGPQDAREVSPEPIVSTVARLKSSLAQPDRRYSEPSMPSSQECLESRVTNQT 396
                                                                                                         ---EQENIDPLHVIENSNAFSTPQTPDIKVSLLGPVTTPEHQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TANG, Junming; EMERLING, Brooke M.;
TANG, Y. Ton; BAUGHN, Mariah R.;
LEE, Ernestine A.; RAMKUMAR, Jayalaxmi;
YUE, Henry; GRIFFIN, Jennifer A.;
YUE, Henry; GRIFFIN, Jennifer A.;
GHAWLA, Narinder K.; TRAN, Bao
NGUYEN, Danniel B.; KHAN, Farrah A.;
SWARNDHI, Ameena R.; HAFALLA, April J.A.;
SWARNAKER, Anita; GURURAJAN, Rajagopal;
POLICKY, Jennifer L.; YAO, Monique G.;
WAREN, Bridget A.; GIETZEN, Kimberly J.;
ELLIOTT, Vicki S.; LEE, Soo Yeun;
SANJANMAA, Bharati; HONCHELL, Cynthia D.;
FOSSYTHE, Ian J.; GORVAD, Ann E.;
RICHARDSON, Thomas W.; LEE, Sally;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: RICHARDSON, THORMSH W.; LEE, SALLY;
APPLICANT: BARROSO, THORMSH W.; LEE, SALLY;
FILE REPREBRUCE: PF-1002 USN
CURRENT APPLICATION NUMBER: US/10/480,962
CURRENT APPLICATION NUMBER: PCT/USO2/17955
PRIOR PRIOR APPLICATION NUMBER: US 60/297,010
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/297,010
PRIOR FILING DATE: 2001-06-08
PRIOR PELING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/299,998
PRIOR PILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/300,377
PRIOR PILING DATE: 2001-06-21
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2002-01-25
NUMBER: OF SEQ. 1D NOS: 40
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OTHER INFORMATION: Incyte ID No: 71768694CD1
                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 14, Application US/10480962; Publication No. US20060115813A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    397 LTKSEGDFPVPRVGSRLES 415
                                                                                                                                                                                                                                                                              602 LTKN-----TPRFGSKSKS 615
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Best Local Similarity
                                                                                                         540 SQFMMV-
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SEQ ID NO 14
LENGTH: 727
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362 IPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVD--DIHAIC 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 SLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIH 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 LAHLSQYSDENWADPYNLAICFGPTLM-HIPDGQDPVSCQAHINEVIKTIIHHEAIFPS 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      535 PLE----YWSQFMMVEQENIDPLH------VIENSNAFSTPQTPDIKVSLLGPVT---- 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----IPSIVVHCVNEIEQRGLTETGLYRI 386
                                                                81 GEGRL-DFTAWNAAIGGAAGGGGTGLQEQQMSRGDIPIIVDACISFVTQHGLRLEGVYRK 139
                                                                                                                                                                446 AEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHLQRVAQ-SPHTKMDVANLAKVFGPTI 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480 LORVAQ-SPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVV----BRLLSL
                                                                                               387 SGCDRIVKELKEKFLR-VKTVPLLSKVDDIHAICSLLKDFLRNLKEPLLIFRLNRAFMEA
 Gaps
 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 5.3%; Score 171; DB 6; Length 1075; Best Local Similarity 24.1%; Pred. No. 0.0038; Matches 63; Conservative 47; Mismatches 123; Indels 28
74; Indels
                                                                                                                                                                                                                                                                  29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             = Gln or STOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE

1 LOCATION: (179) ... (179)

2 OTHER INFORMATION: Xaa = Ser or Gly

US-10-322-836-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           580 ---TPEHQLLKTPSSSSLSQR 597
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Publication No. US20060150283A1

GENERAL INFORMATION:

APPLICANT: Brover, Vyacheslav

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: 2750-1590F0US2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2005-02-14

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR APPLICATION NUMBER: 50/644,190

PRIOR SEQ ID NOS: 119966

SEQ ID NO 50683

LENGTH: 376
               Sequence 49975, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: POLYpeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR FILING DATE: 2006-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 49975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 QTSPMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIH 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 ESSRPIPLILVKCADYLLLTGLNSPNLFKAEGDRKLIQQLVSAYNQDPRASIPEGVNPVD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 AICSLLKDFLRNLKEPLLFFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 TALILIRVSQKSLIANKADSHSLAMEMAPVIMWREDNRPESYR------302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 MIHLQRVAQ-SPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLP 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
4.8%; Score 156; DB 7; Length 376;
Best Local Similarity 26.0%; Pred. No. 0.0087;
Matches 56; Conservative 33; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536 LEYWSQFMMVEQENIDPLHVIENSNAFSTPQTPDI 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 -EYWRR------PSRSPKKSNDFETATPWDL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: peptide

LOCATION: (1)..(376)

; OTHER INDORMATION: Ceres Seq. ID no. 13647982

US-11-056-355B-50683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | NAME/KEY: peptide
| LOCATION: (1)..(376)
| OTHER INFORMATION: Ceres Seq. ID no. 13647982
| US-11-056-3558-49975
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: prt
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: prt
ORGANISM: Arabidopsis thaliana
US-11-056-355B-49975
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Length 376;

4.8%; Score 156; DB 7; 26.0%; Pred. No. 0.0087;

Query Match Best Local Similarity

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                                             149 ESSRPIPLILUVKCADYLILITGLNSPNLFKAEGDRKLIQQLVSAYNQDPRASIPEGVNPVD 208
                                                                                                  357 QTSPMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIH 416
                                                                                  417 AICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFL 476
                                                                                                                                         477 MIHLORVAQ-SPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLP 535
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38; Gaps
88; Indels
                                                                                                                                                              536 LEYWSQFMMVEQENIDPLHVIENSNAFSTPQTPDI 570
                                                                                                                                                                                                                               -EYWRR------PSRSPKKSNDFETATPWDL 326
56; Conservative 33; Mismatches
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Matches
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